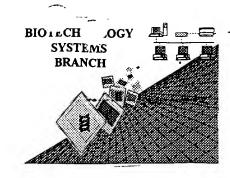# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/596,141

Source: BATCH

Date Processed by STIC: 11/16/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/596,141

DATE: 11/16/2000
TIME: 16:24:35

Input Set : A:\CVT 203.txt
Output Set: N:\CRF3\11162000\I596141.raw

Does Not Comply
Corrected Diskette Needed

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Eva Summary
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PATENT APPLICATION: US/09/596,141   TIME: 16:24:35

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492 Asn Leu Ser Leu Pro Lys Ser Thr Val Asp Lys Met Leu Arg Ala Asp
494              165                 170                 175
498 Val Ile Leu His Lys Val Phe Leu Gln Gly Tyr Gln Leu His Leu Thr
500              180                 185                 190
504 Ser Leu Cys Asn Gly Ser Lys Ser Glu Glu Met Ile Gln Leu Gly Asp
506          195                 200                 205
510 Gln Glu Val Ser Glu Leu Cys Gly Leu Pro Lys Glu Lys Leu Ala Ala
512      210                 215                 220
516 Ala Glu Arg Val Leu Arg Ser Asn Met Asp Ile Leu Lys Pro Ile Leu
518 225                 230                 235                 240
522 Arg Thr Leu Asn Ser Thr Ser Pro Phe Pro Ser Lys Glu Leu Ala Glu
524              245                 250                 255
528 Ala Thr Lys Thr Leu Leu His Ser Leu Gly Thr Leu Ala Gln Glu Leu
530          260                 265                 270
534 Phe Ser Met Arg Ser Trp Ser Asp Met Arg Gln Glu Val Met Phe Leu
536          275                 280                 285
540 Thr Asn Val Asn Ser Ser Ser Ser Thr Gln Ile Tyr Gln Ala Val
542      290                 295                 300
546 Ser Arg Ile Val Cys Gly His Pro Glu Gly Gly Gly Leu Lys Ile Lys
548 305                 310                 315                 320
552 Ser Leu Asn Trp Tyr Glu Asp Asn Asn Tyr Lys Ala Leu Phe Gly Gly
```

FYI!

Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**
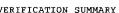
VERIFICATION SUMMARY
PATENT APPLICATION: US/09/596,141

DATE: 11/16/2000
TIME: 16:24:36

Input Set : A:\CVT 203.txt
Output Set: N:\CRF3\11162000\I596141.raw

```
L:25 M:270 C: Current Application Number differs, Replaced Application Number
L:27 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:397 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:397 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:397 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:397 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:397 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:401 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:401 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:401 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:401 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:403 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:403 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:403 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:403 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:1366 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:1366 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:1366 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:1366 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:1366 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:1368 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:1368 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:1368 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:1368 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:1370 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:1370 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:1370 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:1370 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:1372 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:1372 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:1372 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:1372 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:1578 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:1578 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:1578 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:1578 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:1578 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:1582 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:1582 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:1582 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:1582 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:1584 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:1584 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:1584 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:1584 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
```

VERIFICATION SUMMARY   DATE: 11/16/2000
PATENT APPLICATION: US/09/596,141   TIME: 16:24:36

Input Set : A:\CVT 203.txt
Output Set: N:\CRF3\11162000\I596141.raw

```
L:1943 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:1943 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:1943 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:1943 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:1943 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
L:1947 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:1947 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:1947 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:1947 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
M:340 Repeated in SeqNo=7
L:3171 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:3171 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:3171 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
M:340 Repeated in SeqNo=9
```

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION   SERIAL NUMBER: _09/596,141_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid-number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
€400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99